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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/990,415A

DATE: 04/12/2002 P5
TIME: 14:54:27

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04122002\I990415A.raw**

```
      3 <110> APPLICANT: Pharmacia AB
W--> 4 <120> TITLE OF INVENTION: Protein Cluster I
W--> 5 <130> FILE REFERENCE: 00349
W--> 6 <140> CURRENT APPLICATION NUMBER: US/09/990,415A
      7 <141> CURRENT FILING DATE: 2001-11-21
W--> 8 <160> NUMBER OF SEQ ID: 8
      9 <170> SOFTWARE: PatentIn version 3.0
W--> 10 <210> SEQ ID NO: 1
     11 <211> LENGTH: 1232
     12 <212> TYPE: DNA
     13 <213> ORGANISM: human
     15 <220> FEATURE:
     16 <221> NAME/KEY: CDS
     17 <222> LOCATION: (450)..(1232)
     19 <400> SEQUENCE: 1
     20 cccttaggcg ccagggacag ccgagcgtta cctggtcccg ggcagcggag ttctttaccc      60
     22 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggtctggct     120
     24 tgttcccctc cggctcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg     180
     26 aattgccacc cctccctggg cacccttgag gcctccgtgg agggacgtca cggggcagag     240
     28 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat     300
     30 ccccgtgccc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt     360
     32 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag     420
     34 gaaggcggtt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg      473
     35                                    Met Glu Ser Lys Met Gly Glu Leu
     36                                     1               5
     38 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc      521
     39 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
     40     10              15                  20
     42 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg      569
     43 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
     44 25              30                  35                  40
     46 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac      617
     47 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
     48             45                  50                  55
     50 tac agg gcc ggc gtg gtg acc cca ggg atc acc gag gac cag ctg tgg      665
     51 Tyr Arg Ala Gly Val Val Thr Pro Gly Ile Thr Glu Asp Gln Leu Trp
     52             60                  65                  70
     54 agg gcc aag tat gtg tat gac tcc gcc ttc cat ccg gac aca ggg gag      713
     55 Arg Ala Lys Tyr Val Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu
     56         75                  80                  85
     58 aag gtg gtc ctg att ggc cgc atg tca gcc cag gtg ccc atg aac atg      761
     59 Lys Val Val Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met
     60         90                  95                  100
```

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```
62 acc atc act ggc tgc atg ctc aca ttc tac agg aag acc cca acc gtg          809
63 Thr Ile Thr Gly Cys Met Leu Thr Phe Tyr Arg Lys Thr Pro Thr Val
64 105             110             115             120
66 gtg ttc tgg cag tgg gtg aat cag tcc ttc aat gcc att gtt aac tac          857
67 Val Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val Asn Tyr
68             125             130             135
70 tcc aac cgc agt ggt gac act·ccc atc act gtg agg cag ctg ggg aca          905
71 Ser Asn Arg Ser Gly Asp Thr Pro Ile Thr Val Arg Gln Leu Gly Thr
72             140             145             150
74 gcc tat gtg agt gcc acc act gga gct gtg gcc acg gcc ctg gga ctc          953
75 Ala Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu
76             155             160             165
78 aaa tcc ctc acc aag cac ctg ccc ccc ttg gtc ggc aga ttt gtg ccc         1001
79 Lys Ser Leu Thr Lys His Leu Pro Pro Leu Val Gly Arg Phe Val Pro
80     170             175             180
82 ttt gca gca gtg gca gct gcc aac tgc atc aac atc ccc ctg atg agg         1049
83 Phe Ala Ala Val Ala Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg
84 185             190             195             200
86 cag aga gag ctg cag gtg ggc atc ccg gtg gct gat gag gca ggt cag         1097
87 Gln Arg Glu Leu Gln Val Gly Ile Pro Val Ala Asp Glu Ala Gly Gln
88             205             210             215
90 agg ctt ggc tac tcg gtg act gca gcc aag cag gga atc ttc cag gtg         1145
91 Arg Leu Gly Tyr Ser Val Thr Ala Ala Lys Gln Gly Ile Phe Gln Val
92             220             225             230
94 gtg att tca aga atc tgc atg gcg att cct gcc atg gcc atc cca cca         1193
95 Val Ile Ser Arg Ile Cys Met Ala Ile Pro Ala Met Ala Ile Pro Pro
96             235             240             245
98 ctg atc atg gac act ctg gag aag aaa gac ttc ctg aag                     1232
99 Leu Ile Met Asp Thr Leu Glu Lys Lys Asp Phe Leu Lys
100     250             255             260
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 261
105 <212> TYPE: PRT
106 <213> ORGANISM: human
107 <400> SEQUENCE: 2
108 Met Glu Ser Lys Met Gly Glu Leu Pro Leu Asp Ile Asn Ile Gln Glu
109 1           5               10              15
111 Pro Arg Trp Asp Gln Ser Thr Phe Leu Gly Arg Ala Arg His Phe Phe
112             20              25              30
114 Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
115             35              40              45
117 Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Ala Gly Val Val Thr Pro
118     50              55              60
120 Gly Ile Thr Glu Asp Gln Leu Trp Arg Ala Lys Tyr Val Tyr Asp Ser
121 65              70              75              80
123 Ala Phe His Pro Asp Thr Gly Glu Lys Val Val Leu Ile Gly Arg Met
124             85              90              95
126 Ser Ala Gln Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Leu Thr
127             100             105             110
```

W--> 107 at line before `<400> SEQUENCE: 2`

```
129 Phe Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln
130         115             120             125
132 Ser Phe Asn Ala Ile Val Asn Tyr Ser Asn Arg Ser Gly Asp Thr Pro
133         130             135             140
135 Ile Thr Val Arg Gln Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly
136 145             150             155             160
138 Ala Val Ala Thr Ala Leu Gly Leu Lys Ser Leu Thr Lys His Leu Pro
139             165             170             175
141 Pro Leu Val Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn
142             180             185             190
144 Cys Ile Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Gln Val Gly Ile
145         195             200             205
147 Pro Val Ala Asp Glu Ala Gly Gln Arg Leu Gly Tyr Ser Val Thr Ala
148         210             215             220
150 Ala Lys Gln Gly Ile Phe Gln Val Val Ile Ser Arg Ile Cys Met Ala
151 225             230             235             240
153 Ile Pro Ala Met Ala Ile Pro Pro Leu Ile Met Asp Thr Leu Glu Lys
154             245             250             255
156 Lys Asp Phe Leu Lys
157             260
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 1061
162 <212> TYPE: DNA
163 <213> ORGANISM: human
```

W--> `164 <220> FEATURE:`
```
165 <221> NAME/KEY: CDS
166 <222> LOCATION: (450)..(680)
```
W--> `167 <400> SEQUENCE: 3`
```
168 ccccttaggcg ccagggacag ccgagcgtta cctggtcccg ggcagcggag ttctttaccc   60
170 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggtctggct  120
172 tgttcccctc cggctcgaac cacctcttct ctgagccgag ccagctaccg gggctcctgg  180
174 aattgccacc cctccctggg cacccttgag gcctccgtgg agggacgtca cggggcagag  240
176 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat  300
178 ccccgtgccc accgggtggg cgcggccggg aagctcctgc ccctccctgc tggtcggcgt  360
180 cacgcgtgac gtcccgcgtg atggctggga gggcccggcg gcgacagcgg aggcagagag  420
182 gaaggcggtt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg  473
183                                 Met Glu Ser Lys Met Gly Glu Leu
184                                  1               5
186 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc  521
187 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
188  10              15              20
190 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg  569
191 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
192  25              30              35              40
194 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac  617
195 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
196             45              50              55
198 tac agg aag acc cca acc gtg gtg ttc tgg cag tgg gtg aat cag tcc  665
199 Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln Ser
```

```
200            60              65              70
202 ttc aat gcc att gtt aactactcca accgcagtgg tgacactccc atcactgtga      720
203 Phe Asn Ala Ile Val
204         75
206 ggcagctggg gacagcctat gtgagtgcca ccactggagc tgtggccacg gccctgggac      780
208 tcaaatccct caccaagcac ctgcccccct tggtcggcag atttgtgccc tttgcagcag      840
210 tggcagctgc caactgcatc aacatccccc tgatgaggca gagagagctg caggtgggca      900
212 tcccggtggc tgatgaggca ggtcagaggc ttggctactc ggtgactgca gccaagcagg      960
214 gaatcttcca ggtggtgatt tcaagaatct gcatggcgat tcctgccatg gccatcccac     1020
216 cactgatcat ggacactctg gagaagaaag acttcctgaa g                         1061
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 77
221 <212> TYPE: PRT
222 <213> ORGANISM: human
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W--> 223 <400> SEQUENCE: 4
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224 Met Glu Ser Lys Met Gly Glu Leu Pro Leu Asp Ile Asn Ile Gln Glu
225 1               5               10              15
227 Pro Arg Trp Asp Gln Ser Thr Phe Leu Gly Arg Ala Arg His Phe Phe
228         20              25              30
230 Thr Val Thr Asp Pro Arg Asn Leu Leu Leu Ser Gly Ala Gln Leu Glu
231         35              40              45
233 Ala Ser Arg Asn Ile Val Gln Asn Tyr Arg Lys Thr Pro Thr Val Val
234     50              55              60
236 Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val
237 65              70              75
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 1567
242 <212> TYPE: DNA
243 <213> ORGANISM: human
```
W--> 244 <220> FEATURE:
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245 <221> NAME/KEY: CDS
246 <222> LOCATION: (47)..(1015)
```
W--> 247 <400> SEQUENCE: 5
```
248 gggcatttgt cccgggacca ggtccacagt tttatgtgtg agcaag atg gag gct       55
249                                                      Met Glu Ala
250                                                      1
252 gac ctg tct ggc ttt aac atc gat gcc ccc cgt tgg gac cag cgc acc      103
253 Asp Leu Ser Gly Phe Asn Ile Asp Ala Pro Arg Trp Asp Gln Arg Thr
254 5               10              15
256 ttc ctg ggg aga gtg aag cac ttc cta aac atc acg gac ccc cgc act      151
257 Phe Leu Gly Arg Val Lys His Phe Leu Asn Ile Thr Asp Pro Arg Thr
258 20              25              30              35
260 gtc ttt gta tct gag cgg gag ctg gac tgg gcc aag gtg atg gtg gag      199
261 Val Phe Val Ser Glu Arg Glu Leu Asp Trp Ala Lys Val Met Val Glu
262             40              45              50
264 aag agc agg atg ggg gtt gtg ccc cca ggc acc caa gtg gag cag ctg      247
265 Lys Ser Arg Met Gly Val Val Pro Pro Gly Thr Gln Val Glu Gln Leu
266         55              60              65
268 ctg tat gcc aag aag ctg tat gac tcg gcc ttc cac ccc gac act ggg      295
```

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```
269 Leu Tyr Ala Lys Lys Leu Tyr Asp Ser Ala Phe His Pro Asp Thr Gly
270         70            75            80
272 gag aag atg aat gtc atc ggg cgc atg tct ttc cag ctt cct ggc ggc   343
273 Glu Lys Met Asn Val Ile Gly Arg Met Ser Phe Gln Leu Pro Gly Gly
274     85            90            95
276 atg atc atc acg ggc ttc atg ctc cag ttc tac agg acg atg ccg gcg   391
277 Met Ile Ile Thr Gly Phe Met Leu Gln Phe Tyr Arg Thr Met Pro Ala
278 100           105           110           115
280 gtg atc ttc tgg cag tgg gtg aac cag tcc ttc aat gcc tta gtc aac   439
281 Val Ile Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Leu Val Asn
282           120           125           130
284 tac acc aac agg aat gcg gct tcc ccc aca tca gtc agg cag atg gcc   487
285 Tyr Thr Asn Arg Asn Ala Ala Ser Pro Thr Ser Val Arg Gln Met Ala
286         135           140           145
288 ctt tcc tac ttc aca gcc aca acc act gct gtg gcc acg gct gtg ggc   535
289 Leu Ser Tyr Phe Thr Ala Thr Thr Thr Ala Val Ala Thr Ala Val Gly
290         150           155           160
292 atg aac atg ttg aca aag aaa gcg ccg ccc ttg gtg ggc cgc tgg gtg   583
293 Met Asn Met Leu Thr Lys Lys Ala Pro Pro Leu Val Gly Arg Trp Val
294     165           170           175
296 ccc ttt gcc gct gtg gct gcg gct aac tgt gtc aat atc ccc atg atg   631
297 Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Val Asn Ile Pro Met Met
298 180           185           190           195
300 cga cag agg gag ctc ata aag gga atc tgc gtg aag gac agg aat gaa   679
301 Arg Gln Arg Glu Leu Ile Lys Gly Ile Cys Val Lys Asp Arg Asn Glu
302         200           205           210
304 aat gag att ggt cat tcc cgg aga gct gcg gcc ata ggc atc acc caa   727
305 Asn Glu Ile Gly His Ser Arg Arg Ala Ala Ala Ile Gly Ile Thr Gln
306         215           220           225
308 gta gtt att tct cgg atc acc atg tca gct cct ggg atg atc ttg ctg   775
309 Val Val Ile Ser Arg Ile Thr Met Ser Ala Pro Gly Met Ile Leu Leu
310         230           235           240
312 cca gtc atc atg gaa agg ctt gag aaa ttg cac ttc atg cag aaa gtc   823
313 Pro Val Ile Met Glu Arg Leu Glu Lys Leu His Phe Met Gln Lys Val
314     245           250           255
316 aag gtc ctg cac gcc cca ttg cag gtc atg ctg agc ggg tgc ttc ctc   871
317 Lys Val Leu His Ala Pro Leu Gln Val Met Leu Ser Gly Cys Phe Leu
318 260           265           270           275
320 atc ttc atg gtg cca gtg gcg tgt ggg ctt ttc cca cag aaa tgt gaa   919
321 Ile Phe Met Val Pro Val Ala Cys Gly Leu Phe Pro Gln Lys Cys Glu
322         280           285           290
324 ttg cca gtt tcc tat ctg gaa ccg aag ctc caa gac act atc aag gcc   967
325 Leu Pro Val Ser Tyr Leu Glu Pro Lys Leu Gln Asp Thr Ile Lys Ala
326         295           300           305
328 aag tat gga gaa ctt gag cct tat gtc tac ttc aat aag ggt ctc taa  1015
329 Lys Tyr Gly Glu Leu Glu Pro Tyr Val Tyr Phe Asn Lys Gly Leu
330         310           315           320
332 atgccccact tcagcaagga ccagtctatt cccatattca ccagctcctc cttagctacg  1075
334 tgcacacttg tgtcctcctt cccctttgcc aacaaggcct gaaggccagg gtagattggg  1135
```

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```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:107 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:223 M:283 W: Missing Blank Line separator, <400> field identifier
L:244 M:283 W: Missing Blank Line separator, <220> field identifier
L:247 M:283 W: Missing Blank Line separator, <400> field identifier
L:357 M:283 W: Missing Blank Line separator, <400> field identifier
L:425 M:283 W: Missing Blank Line separator, <220> field identifier
L:428 M:283 W: Missing Blank Line separator, <220> field identifier
L:432 M:283 W: Missing Blank Line separator, <400> field identifier
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:564 M:283 W: Missing Blank Line separator, <220> field identifier
L:568 M:283 W: Missing Blank Line separator, <400> field identifier
```